

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

Ciossek, Thomas
Ullrich, Axel
Millauer, Birgit

(ii) TITLE OF INVENTION:

METHODS FOR DIAGNOSIS
AND TREATMENT OF MDK1
SIGNAL TRANSDUCTION
DISORDERS

(iii) NUMBER OF SEQUENCES:

12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:

(B) STREET:

Lyon & Lyon
633 West Fifth Street
Suite 4700
Los Angeles
California
U.S.A.
90071-2066

(C) CITY:

(D) STATE:

(E) COUNTRY:

(F) ZIP:

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE:

3.5" Diskette, 1.44 Mb
storage
IBM Compatible
IBM P.C. DOS 5.0
Word Perfect 5.1

(B) COMPUTER:

(C) OPERATING SYSTEM:

(D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

08/368,776

(B) FILING DATE:

January 3, 1995

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

Prior applications total,
including application
described below:

none

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Ciossek, Thomas
Ullrich, Axel
Millauer, Birgit

(ii) TITLE OF INVENTION: METHODS FOR DIAGNOSIS
AND TREATMENT OF MDK1
SIGNAL TRANSDUCTION
DISORDERS

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Lyon & Lyon
(B) STREET: 633 West Fifth Street
Suite 4700
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 90071-2066

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: Word Perfect 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/368,776
(B) FILING DATE: January 3, 1995
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

Prior applications total,
including application
described below: none

- (A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Warburg, Richard J.
(B) REGISTRATION NUMBER: 32,327
(C) REFERENCE/DOCKET NUMBER: 208/007

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (213) 489-1600
(B) TELEFAX: (213) 955-0440
(C) TELEX: 67-3510

(2) INFORMATION FOR SEQUENCE ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4304 base pairs
(B) TYPE: nucleic acid
(C) STRANDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AAGCGGCCGG TCTGCAGTCG GAGACTTGCA GGCAGCAAAC ACGGTGCGAA 50
CGAACCGGAG GGGGGAGAGA GAAATCAAAC AGCTAAGCGT GGAGCAGACG 100
GCCTGGGACC CAGAAGGGGA TCGATGCGAG GAGCGCAATA ATAACAACAA 150
TAATAACCCA CTTCGGAGCA AACAGCATCT AAAGAGCTGC GACCCAACTG 200
CAGCCTAAAA AAATCAAACC TGCTCATGCA CCATGGTTGT TCAAACCTCGG 250
TTCCCTTCGT GGATTATTTT GTGTTACATC TGGCTGCTTG GCTTTGCACA 300
CACGGGGGAG GCGCAGGCTG CGAAGGAAGT ACTATTACTG GACTCGAAAG 350
CACAACAAAC AGAATTGGAA TGGATTCCT CTCCACCCAG TGGGTGGGAA 400
GAAATTAGTG GTTTGGATGA GAACTACACT CCGATAAGAA CATACCAGGT 450
GTGCCAGGTC ATGGAGCCCA ACCAGAACAA CTGGCTGCGG ACTAACTGGA 500
TTTCTAAAGG CAACGCACAA AGGATTTTGT TAGAATTGAA ATTCACCTTG 550
AGGGATTGTA ATAGTCTTCC CGGAGTCCTG GGAACCTGCA AGGAAACGTT 600

TAATTTGTAC TATTATGAAA CAGACTACGA CACCGGCAGG AATATACGAG 650
 AAAACCTTTA TGTTAAAATA GACACCATTG CTGCAGATGA AAGTTTCACA 700
 CAAGGTGACC TTGGTGAAAAG AAAGATGAAG CTGAACACTG AGGTGAGAGA 750
 GATTGGACCT TTGTCCAAAA AGGGATTCTA TCTTGCCTTT CAGGATGTAG 800
 GGGCTTGCAT AGCATTGGTT TCTGTCAAAG TGTACTACAA GAAGTGCTGG 850
 ACCATTGTTG AGAACTTAGC TGTCTTTCCA GATACAGTGA CTGGTTCGGA 900
 ATTTTCCTCC TTAGTCGAGG TCCGTGGGAC ATGTGTCAGC AGTGCCGAGG 950
 AAGAGGCAGA AAATTCCCCC AGAATGCATT GCAGTGCAGA AGGAGAGTGG 1000
 CTAGTACCCA TTGGAAAATG CATCTGCAAA GCAGGCTATC AGCAAAAAGG 1050
 GGACACTTGC GAACCCTGTG GCCGCAGGTT CTACAAATCT TCCTCTCAGG 1100
 ATCTCCAGTG TTCTCGTTGT CCAACCCACA GCTTCTCTGA CCGAGAAGGA 1150
 TCATCCAGGT GTGAATGTGA AGATGGGTAC TACAGAGCTC CTTCTGATCC 1200
 ACCATACGTT GCATGCACGA GGCCTCCCTC TGCACCACAG AACCTTATTT 1250
 TCAATATCAA TCAAACGACT GTAAGTTTGG AATGGAGTCC TCCGGCTGAC 1300
 AACGGGGGAA GAAACGATGT CACCTACAGA ATACTGTGTA AGCGGTGCAG 1350
 TTGGGAACAG GGAGAATGTG TGCCATGCGG AAGTAACATT GGATACATGC 1400
 CCCAGCAGAC GGGATTAGAG GATAACTATG TCACTGTCAT GGACCTACTT 1450
 GCCCATGCAA ATTACACTTT CGAAGTTGAA GCTGTAAATG GAGTTTCGGA 1500
 CTTAAGCAGA TCCCAGAGGC TCTTCGCTGC TGTTAGCATC ACCACCGGTC 1550
 AAGCAGCTCC CTCGCAAGTG AGTGGAGTCA TGAAGGAGCG AGTACTGCAG 1600
 CGGAGTGTGC AGCTTTCCTG GCAGGAGCCG GAGCATCCCA ATGGAGTCAT 1650
 CACGGAATAT GAAATCAAGT ATTATGAGAA AGATCAACGG GAAAGGACGT 1700
 ACTCAACACT CAAAACCAAG TCCACCTCCG CCTCCATTAA TAATCTGAAA 1750
 CCGGGAACAG TGTACGTCTT TCAGATCCGG GCGGTCACTG CTGCCGGTTA 1800
 TGGAAACTAC AGCCCTAGGC TTGATGTTGC CACACTTGAG GAAGCTTCAG 1850
 GTAAAATGTT TGAAGCGACA GCAGTCTCCA GTGAACAGAA TCCTGTCATC 1900
 ATAATTGCTG TAGTGGCTGT AGCAGGGACC ATCATCTTGG TGTTCATGGT 1950
 GTTCGGCTTC ATCATTGGAA GAAGGCACTG TGGTTATAGC AAGGCTGACC 2000

AAGAAGGGGA TGAAGAACTC TACTTTTCATT TTAAATTTCC AGGCACCAAA 2050
 ACCTACATTG ACCCTGAAAC CTATGAGGAC CCAAATAGAG CTGTCCATCA 2100
 ATTCGCCAAG GAGCTAGATG CCTCCTGTAT TAAAATTGAG CGTGTGATTG 2150
 GTGCAGGAGA ATTTGGAGAA GTTTGCAGTG GTCGTTTGAA ACTTCCGGGC 2200
 CAGAGAGATG TTGCAGTGGC CATAAAAACC CTGAAAGTTG GTTACACAGA 2250
 AAAGCAAAGG AGGGACTTTT TATGCGAAGC AAGCATCATG GGGCAATTTG 2300
 ACCACCCAAA TGTCGTCCAT TTGGAAGGGG TTGTTACAAG AGGGAAGCCT 2350
 GTCATGATTG TGATAGAGTT CATGGAGAAT GGAGCCCTGG ATGCATTTCT 2400
 CAGGAAACAC GATGGGCAGT TTACAGTCAT TCAGTTGGTA GGAATGTTGA 2450
 GAGGTATTGC CGCTGGGATG CGATACTTGG CTGATATGGG ATACGTTTAC 2500
 AGGGACCTTG CAGCGCGCAA CATCCTTGTC AACAGCAATC TTGTTTGTA 2550
 AGTGTCAGAT TTTGGCCTTT CCCGGGTTAT AGAGGATGAT CCCGAAGCTG 2600
 TCTACACCAC GACTGGTGGG AAAATTCCAG TAAGGTGGAC TGCACCGGAA 2650
 GCCATTCAAT ACCGGAAGTT CACCTCAGCC AGCGATGTGT GGAGCTATGG 2700
 GATTGTCATG TGGGAAGTGA TGTCTTATGG AGAAAGACCT TACTGGGACA 2750
 TGTCAAATCA AGATGTCATT AAAGCGATAG AAGAAGGTTA TCGTTTGCCG 2800
 GCGCCCATGG ATTGCCCAGC TGGTCTTCAC CAGCTAATGC TGGATTGTTG 2850
 GCAGAAAGAT CGGGCGGAAA GGCCAAAGTT TGAGCAGATA GTCGGAATTC 2900
 TAGACAAAAT GATTGAAAC CCAAGTAGTC TGAAAACACC CCTGGGAACT 2950
 TGTAGTAGAC CCTTAAGCCC TCTTCTGGAC CAGAGCACTC CTGACTTCAC 3000
 TGCCTTCTGT TCAGTTGGAG AATGGTTGCA AGCTATTAAA ATGGAAAGGT 3050
 ATAAGGACAA CTTACAGCA GCGGGTTACA ACTCACTCGA GTCAGTGGCC 3100
 AGGATGACTA TCGATGATGT GATGAGTTTA GGGATCACAC TGGTTGGCCA 3150
 TCAAAAGAAG ATCATGAGCA GCATCCAGAC TATGCGGGCA CAAATGTTGC 3200
 ATTTACACGG AACAGGCATC CAAGTGTGAC ACATCGGCCT CCCTCAGATG 3250
 AGGCTTAAGA CTGCAGGAGA ACAGTTCTGG CCTTCAGTAT ACGCATAGAA 3300
 TGCTGCTAGA AGACAGTTGA TATACTGGGT CCTTCCTACA AGAAAGAGAA 3350
 GATTTTAGAA GCACCTCCAG ACTTGAAGTC CTAAGTGCCA CCAGAATATA 3400

CAAAAAGGGA ATTTAGGATC CACCACTGGT GGCCAGGAAC ACAGCAGAGA 3450
 CAATAAACAA AGTACTACCT GAAAAACATC CCAACACCTT GAGCTCTCGA 3500
 ACCTCCTTTT TATCTTATAG ACTTTTAAAA AATGTACATA AAGAATTTAA 3550
 GAAAGAATAT ATTTGTCAAA TAAAAATCAT GATCTTATTG TTAAAATCAA 3600
 TGAAATATTT TCCTTAAAAAT ATGTGATTTT AGACTATTCT TTTCCAGAAC 3650
 CATCTGTGTT TATTCTGCTT AAGGACTTTG TTTTAGAAAG TTATTTGTAG 3700
 CTTTGGACCT TTTTAGTGTT AAATTTATGA CACGTTACTA CACTGGGAAC 3750
 CTTTGAAGAC TCTCAAACTT AAAGGAAAGC AAAACTACGC ACATAGTCGA 3800
 GGATGGACTT TGTCCTTCAT GGCTTTGGTA TCCTGGCTGT GTCATTTTGT 3850
 TAAACCAGTG ATGTTTTTCAT ATTGTTTGCT GATTGGCAGG TAGTTCAAAA 3900
 TTGCAAGTTG CCAAGAGCTC TGATATTTTT TAACAGGATT TTTTTTCTT 3950
 TGTAAAAATC AGATAACATA CTAACTTTTC AATGAAAAAA AAAAAAAAAG 4000
 AAGCAATAAT GATCCATAAA TACTATAAGG CACTTTTAAC AGATTGTTTA 4050
 TAGAGTGATT TACTAGGCAG AATTTAATAA AAAAAAAGA GAGATGTCAA 4100
 ATTTTAGGTT TATGTGTATA TGATAAAAGG CTGAGCTTCG TCTGAAGATG 4150
 CTGGTGAAAG CAAGACTGGA AGCGAAGCTC TCCAGCTTTG GCTAACCCAA 4200
 TCCGAGCACA TCAAGAGCTT CAGTCTTG TG ACAGTAAGAA ATTTAGGAAC 4250
 ATAGTTGACC TATATTTTGT ATTCTTTCTT GTTGAATGCA GTCCAAATAC 4300
 AAAA 4304

(2) INFORMATION FOR SEQUENCE ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 998 amino acids
 (B) TYPE: amino acid
 (C) STRANDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile
 1 5 10 15
 Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu
 20 25 30
 Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile
 35 40 45
 Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn
 50 55 60
 Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn
 65 70 75 80
 Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln
 85 90 95
 Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu
 100 105 110
 Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
 115 120 125
 Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
 130 135 140
 Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
 145 150 155 160
 Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
 165 170 175
 Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
 180 185 190
 Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile
 195 200 205
 Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
 210 215 220
 Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
 225 230 235 240
 Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
 245 250 255
 Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
 260 265 270

Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser
 275 280 285
 Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg
 290 295 300
 Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
 305 310 315 320
 Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
 325 330 335
 Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
 340 345 350
 Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
 355 360 365
 Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
 370 375 380
 Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
 385 390 395 400
 Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
 405 410 415
 Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
 420 425 430
 Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
 435 440 445
 Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln
 450 455 460
 Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
 465 470 475 480
 Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys
 485 490 495
 Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
 500 505 510
 Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro
 515 520 525
 Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Gly Lys Met Phe Glu
 530 535 540
 Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val
 545 550 555 560

Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe
 565 570 575
 Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly
 580 585 590
 Asp Glu Glu Leu Tyr Phe His Phe Lys Phe Pro Gly Thr Lys Thr Tyr
 595 600 605
 Ile Asp Pro Glu Thr Tyr Glu Asp Pro Asn Arg Ala Val His Gln Phe
 610 615 620
 Ala Lys Glu Leu Asp Ala Ser Cys Ile Lys Ile Glu Arg Val Ile Gly
 625 630 635 640
 Ala Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Gly
 645 650 655
 Gln Arg Asp Val Ala Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr
 660 665 670
 Glu Lys Gln Arg Arg Asp Phe Leu Cys Glu Ala Ser Ile Met Gly Gln
 675 680 685
 Phe Asp His Pro Asn Val Val His Leu Glu Gly Val Val Thr Arg Gly
 690 695 700
 Lys Pro Val Met Ile Val Ile Glu Phe Met Glu Asn Gly Ala Leu Asp
 705 710 715 720
 Ala Phe Leu Arg Lys His Asp Gly Gln Phe Thr Val Ile Gln Leu Val
 725 730 735
 Gly Met Leu Arg Gly Ile Ala Ala Gly Met Arg Tyr Leu Ala Asp Met
 740 745 750
 Gly Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser
 755 760 765
 Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Ile Glu
 770 775 780
 Asp Asp Pro Glu Ala Val Tyr Thr Thr Thr Gly Gly Lys Ile Pro Val
 785 790 795 800
 Arg Trp Thr Ala Pro Glu Ala Ile Gln Tyr Arg Lys Phe Thr Ser Ala
 805 810 815
 Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr
 820 825 830
 Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala
 835 840 845

Ile Glu Glu Gly Tyr Arg Leu Pro Ala Pro Met Asp Cys Pro Ala Gly
 850 855 860
 Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Asp Arg Ala Glu Arg
 865 870 875 880
 Pro Lys Phe Glu Gln Ile Val Gly Ile Leu Asp Lys Met Ile Arg Asn
 885 890 895
 Pro Ser Ser Leu Lys Thr Pro Leu Gly Thr Cys Ser Arg Pro Leu Ser
 900 905 910
 Pro Leu Leu Asp Gln Ser Thr Pro Asp Phe Thr Ala Phe Cys Ser Val
 915 920 925
 Gly Glu Trp Leu Gln Ala Ile Lys Met Glu Arg Tyr Lys Asp Asn Phe
 930 935 940
 Thr Ala Ala Gly Tyr Asn Ser Leu Glu Ser Val Ala Arg Met Thr Ile
 945 950 955 960
 Asp Asp Val Met Ser Leu Gly Ile Thr Leu Val Gly His Gln Lys Lys
 965 970 975
 Ile Met Ser Ser Ile Gln Thr Met Arg Ala Gln Met Leu His Leu His
 980 985 990
 Gly Thr Gly Ile Gln Val
 995

(2) INFORMATION FOR SEQUENCE ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 610 amino acids
 (B) TYPE: amino acid
 (C) STRANDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile
 1 5 10 15
 Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu
 20 25 30
 Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile
 35 40 45

Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn
 50 55 60
 Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn
 65 70 75 80
 Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln
 85 90 95
 Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu
 100 105 110
 Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
 115 120 125
 Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
 130 135 140
 Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
 145 150 155 160
 Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
 165 170 175
 Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
 180 185 190
 Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile
 195 200 205
 Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
 210 215 220
 Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
 225 230 235 240
 Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
 245 250 255
 Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
 260 265 270
 Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser
 275 280 285
 Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg
 290 295 300
 Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
 305 310 315 320
 Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
 325 330 335

Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
 340 345 350
 Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
 355 360 365
 Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
 370 375 380
 Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
 385 390 395 400
 Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
 405 410 415
 Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
 420 425 430
 Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
 435 440 445
 Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln
 450 455 460
 Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
 465 470 475 480
 Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys
 485 490 495
 Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
 500 505 510
 Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro
 515 520 525
 Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Gly Lys Met Phe Glu
 530 535 540
 Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val
 545 550 555 560
 Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe
 565 570 575
 Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly
 580 585 590
 Asp Glu Glu Leu Tyr Phe His Ser Leu Val Thr Asn Glu His Leu Ser
 595 600 605
 Val Leu
 610

114

B

(2) INFORMATION FOR SEQUENCE ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2901 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AAGCGGCCGG TCTGCAGTCG GAGACTTGCA GGCAGCAAAC ACGGTGCGAA 50
 CGAACCGGAG GGGGGAGAGA GAAATCAAAC AGCTAAGCGT GGAGCAGACG 100
 GCCTGGGACC CAGAAGGGGA TCGATGCGAG GAGCGCAATA ATAACAACAA 150
 TAATAACCCA CTTCGGAGCA AACAGCATCT AAAGAGCTGC GACCCAACCTG 200
 CAGCCTAAAA AAATCAAACC TGCTCATGCA CCATGGTTGT TCAAACCTCGG 250
 TTCCCTTCGT GGATTATTTT GTGTTACATC TGGCTGCTTG GCTTTGCACA 300
 CACGGGGGAG GCGCAGGCTG CGAAGGAAGT ACTATTACTG GACTCGAAAG 350
 CACAACAAAC AGAATTGGAA TGGATTTCCT CTCCACCCAG TGGGTGGGAA 400
 GAAATTAGTG GTTTGGATGA GAACTACACT CCGATAAGAA CATAACAGGT 450
 GTGCCAGGTC ATGGAGCCCA ACCAGAACAA CTGGCTGCGG ACTAACTGGA 500
 TTTCTAAAGG CAACGCACAA AGGATTTTGT TAGAATTGAA ATTCACCTTG 550
 AGGGATTGTA ATAGTCTTCC CGGAGTCCTG GGAACCTTGCA AGGAAACGTT 600
 TAATTGTAC TATTATGAAA CAGACTACGA CACCGGCAGG AATATACGAG 650
 AAAACCTTTA TGTAAAATA GACACCATTG CTGCAGATGA AAGTTTCACA 700
 CAAGGTGACC TTGGTGAAAG AAAGATGAAG CTGAACACTG AGGTGAGAGA 750
 GATTGGACCT TTGTCCAAAA AGGGATTCTA TCTTGCCCTT CAGGATGTAG 800
 GGGCTTGCAT AGCATTGGTT TCTGTCAAAG TGTACTACAA GAAGTGCTGG 850
 ACCATTGTTG AGAACTTAGC TGTCTTTCCA GATACAGTGA CTGGTTCGGA 900
 ATTTTCCTCC TTAGTCGAGG TCCGTGGGAC ATGTGTCAGC AGTGCCGAGG 950
 AAGAGGCAGA AAATCCCCC AGAATGCATT GCAGTGCAGA AGGAGAGTGG 1000
 CTAGTACCCA TTGAAAATG CATCTGCAA GCAGGCTATC AGCAAAAAGG 1050

GGACACTTGC GAACCCTGTG GCCGCAGGTT CTACAAATCT TCCTCTCAGG 1100
ATCTCCAGTG TTCTCGTTGT CCAACCCACA GCTTCTCTGA CCGAGAAGGA 1150
TCATCCAGGT GTGAATGTGA AGATGGGTAC TACAGAGCTC CTTCTGATCC 1200
ACCATACGTT GCATGCACGA GGCCTCCCTC TGCACCACAG AACCTTATTT 1250
TCAATATCAA TCAAACGACT GTAAGTTTGG AATGGAGTCC TCCGGCTGAC 1300
AACGGGGGAA GAAACGATGT CACCTACAGA ATACTGTGTA AGCGGTGCAG 1350
TTGGGAACAG GGAGAATGTG TGCCATGCGG AAGTAACATT GGATACATGC 1400
CCCAGCAGAC GGGATTAGAG GATAACTATG TCACTGTCAT GGACCTACTT 1450
GCCCATGCAA ATTACACTTT CGAAGTTGAA GCTGTAAATG GAGTTTCGGA 1500
CTTAAGCAGA TCCCAGAGGC TCTTCGCTGC TGTTAGCATC ACCACCGGTC 1550
AAGCAGCTCC CTCGCAAGTG AGTGGAGTCA TGAAGGAGCG AGTACTGCAG 1600
CGGAGTGTGC AGCTTTCCTG GCAGGAGCCG GAGCATCCCA ATGGAGTCAT 1650
CACGGAATAT GAAATCAAGT ATTATGAGAA AGATCAACGG GAAAGGACGT 1700
ACTCAACACT CAAAACCAAG TCCACCTCCG CCTCCATTAA TAATCTGAAA 1750
CCGGGAACAG TGTACGTCTT TCAGATCCGG GCGGTCACTG CTGCCGGTTA 1800
TGGAAACTAC AGCCCTAGGC TTGATGTTGC CACACTTGAG GAAGCTTCAG 1850
GTAAAATGTT TGAAGCGACA GCAGTCTCCA GTGAACAGAA TCCTGTCATC 1900
ATAATTGCTG TAGTGGCTGT AGCAGGGACC ATCATCTTGG TGTTTCATGGT 1950
GTTCGGCTTC ATCATTGGAA GAAGGCACTG TGGTTATAGC AAGGCTGACC 2000
AAGAAGGGGA TGAAGAACTC TACTTTCATT CTTTAGTAAC AAATGAGCAC 2050
CTGTCAGTTT TATAAACCGC AACAATAACT GTTTAAGACA ATCAATTTTG 2100
GATAACAAT CAACTACAGC AGAATAAATC AAGATTTTAA AGTCCCATT 2150
TCCTTTATAC ATTCTGCTTA TTTTGTGTGTT ATATGTTTAT TTTTAAACT 2200
CTGATCTTGA TTGAATGTGA TACCATAAGC ACAGTTAGGC TGCAGTGTA 2250
ATATATAAAG ACATTGTTCT GAGAGCAGTA CGATTTTCATG GAAAGATTGT 2300
TTGGTGGCTT TGTTAAAATT AATAAAGAAT TTTTAAGGAT ATAGTGTAAT 2350
TTTCTTCATT GCATTAATAT AACCAAATAT GCCTACCTAT CTTTGTCTTG 2400
AACCAAATGA ATAGATTTGG AATACTTTAT TGTAATTGAA TTTGATATAA 2450

AGTTGACTGA GCATTTATGT GTTACCTGCA TGCTTCTGGG TGCATTGAAA 2500
 TATTTTAACT TTAAAATGA TACTATGTTG TTTCAATTTT GACTACCTTT 2550
 TGTGAGGCAT ACTGGCTACC TCCTCCTATT AGCTAAGATC TTCCAAAGCC 2600
 TTATAATGAA AAGTTTATAT AAACCATTTC TCTTTCAAAT CACTGTCATA 2650
 CTTGGTCACG GATCCCAGGA ATATTGTAAA TTTTCTAATT TACTCTGCAC 2700
 TTTGTATATC CAGCCTCTAT TACCCTCAAG GTGAATATAA AACTATGTCT 2750
 TTTGAATATT TCTCTTTGAT TTTGTGATAG CAGTCCCTCA TATCTTGTCAC 2800
 TAATTTTATG TATATGTCAA CAGTGGTTGG TCTTTAAAAA TAAATCAAAG 2850
 AATAAGTAAA AAAAAAAAAA AAAAAAAAAA AAAAATAAAA AAAAAAAAAA 2900
 A 2901

(2) INFORMATION FOR SEQUENCE ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 626 amino acids
 (B) TYPE: amino acid
 (C) STRANDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile
 1 5 10 15
 Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu
 20 25 30
 Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile
 35 40 45
 Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn
 50 55 60
 Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn
 65 70 75 80
 Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln
 85 90 95
 Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu
 100 105 110

Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
 115 120 125
 Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
 130 135 140
 Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
 145 150 155 160
 Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
 165 170 175
 Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
 180 185 190
 Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile
 195 200 205
 Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
 210 215 220
 Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
 225 230 235 240
 Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
 245 250 255
 Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
 260 265 270
 Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser
 275 280 285
 Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg
 290 295 300
 Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
 305 310 315 320
 Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
 325 330 335
 Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
 340 345 350
 Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
 355 360 365
 Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
 370 375 380
 Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
 385 390 395 400

Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
 405 410 415
 Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
 420 425 430
 Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
 435 440 445
 Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln
 450 455 460
 Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
 465 470 475 480
 Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys
 485 490 495
 Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
 500 505 510
 Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro
 515 520 525
 Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Gly Lys Met Phe Glu
 530 535 540
 Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val
 545 550 555 560
 Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe
 565 570 575
 Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly
 580 585 590
 Asp Glu Glu Leu Tyr Phe His Ser Leu Tyr Arg Glu Arg Gly Asp Gly
 595 600 605
 Met Glu Lys Thr Gln His Asn Lys Lys Trp Met Ile Ala Ser Cys Ser
 610 615 620
 Arg Leu
 625

(2) INFORMATION FOR SEQUENCE ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AAGCGGCCGG TCTGCAGTCG GAGACTTGCA GGCAGCAAAC ACGGTGCGAA 50
 CGAACCGGAG GGGGGAGAGA GAAATCAAAC AGCTAAGCGT GGAGCAGACG 100
 GCCTGGGACC CAGAAGGGGA TCGATGCGAG GAGCGCAATA ATAACAACAA 150
 TAATAACCCA CTTCGGAGCA AACAGCATCT AAAGAGCTGC GACCCAACTG 200
 CAGCCTAAAA AAATCAAACC TGCTCATGCA CCATGGTTGT TCAAACCTCGG 250
 TTCCCTTCGT GGATTATTTT GTGTTACATC TGGCTGCTTG GCTTTGCACA 300
 CACGGGGGAG GCGCAGGCTG CGAAGGAAGT ACTATTACTG GACTCGAAAG 350
 CACAACAAAC AGAATTGGAA TGGATTTCCT CTCCACCCAG TGGGTGGGAA 400
 GAAATTAGTG GTTTGGATGA GAACTACACT CCGATAAGAA CATACCAGGT 450
 GTGCCAGGTC ATGGAGCCCA ACCAGAACAA CTGGCTGCGG ACTAACTGGA 500
 TTTCTAAAGG CAACGCACAA AGGATTTTGT TAGAATTGAA ATTCACCTTG 550
 AGGGATTGTA ATAGTCTTCC CGGAGTCCTG GGAACCTGCA AGGAAACGTT 600
 TAATTTGTAC TATTATGAAA CAGACTACGA CACCGGCAGG AATATACGAG 650
 AAAACCTTTA TGTTAAAATA GACACCATTG CTGCAGATGA AAGTTTCACA 700
 CAAGGTGACC TTGGTGAAAG AAAGATGAAG CTGAACACTG AGGTGAGAGA 750
 GATTGGACCT TTGTCCAAAA AGGGATTCTA TCTTGCCTTT CAGGATGTAG 800
 GGGCTTGCAT AGCATTGGTT TCTGTCAAAG TGTACTACAA GAAGTGCTGG 850
 ACCATTGTTG AGAACTTAGC TGTCTTTCCA GATACAGTGA CTGGTTCGGA 900
 ATTTTCCTCC TTAGTCGAGG TCCGTGGGAC ATGTGTCAGC AGTGCCGAGG 950
 AAGAGGCAGA AAATTCCCCC AGAATGCATT GCAGTGCAGA AGGAGAGTGG 1000
 CTAGTACCCA TTGGAAAATG CATCTGCAAA GCAGGCTATC AGCAAAAAGG 1050
 GGACACTTGC GAACCCTGTG GCCGCAGGTT CTACAAATCT TCCTCTCAGG 1100
 ATCTCCAGTG TTCTCGTTGT CCAACCCACA GCTTCTCTGA CCGAGAAGGA 1150
 TCATCCAGGT GTGAATGTGA AGATGGGTAC TACAGAGCTC CTTCTGATCC 1200
 ACCATACGTT GCATGCACGA GGCCTCCCTC TGCACCACAG AACCTTATTT 1250
 TCAATATCAA TCAAACGACT GTAAGTTTGG AATGGAGTCC TCCGGCTGAC 1300

AACGGGGGAA GAAACGATGT CACCTACAGA ATACTGTGTA AGCGGTGCAG 1350
TTGGGAACAG GGAGAATGTG TGCCATGCGG AAGTAACATT GGATACATGC 1400
CCCAGCAGAC GGGATTAGAG GATAACTATG TCACTGTCAT GGACCTACTT 1450
GCCCCATGCAA ATTACACTTT CGAAGTTGAA GCTGTAAATG GAGTTTCGGA 1500
CTTAAGCAGA TCCCAGAGGC TCTTCGCTGC TGTTAGCATC ACCACCGGTC 1550
AAGCAGCTCC CTCGCAAGTG AGTGGAGTCA TGAAGGAGCG AGTACTGCAG 1600
CGGAGTGTGC AGCTTTCCTG GCAGGAGCCG GAGCATCCCA ATGGAGTCAT 1650
CACGGAATAT GAAATCAAGT ATTATGAGAA AGATCAACGG GAAAGGACGT 1700
ACTCAACACT CAAAACCAAG TCCACCTCCG CCTCCATTAA TAATCTGAAA 1750
CCGGGAACAG TGTACGTCTT TCAGATCCGG GCGGTCACTG CTGCCGGTTA 1800
TGGAAGTAC AGCCCTAGGC TTGATGTTGC CACACTTGAG GAAGCTTCAG 1850
GTAAATGTT TGAAGCGACA GCAGTCTCCA GTGAACAGAA TCCTGTCATC 1900
ATAATTGCTG TAGTGGCTGT AGCAGGGACC ATCATCTTGG TGTTTCATGGT 1950
GTTCCGGCTTC ATCATTGGAA GAAGGCACTG TGGTTATAGC AAGGCTGACC 2000
AAGAAGGGGA TGAAGAACTC TACTTTCATT CTCTTTACAG GGAAAGGGGA 2050
GACGGGATGG AAAAGACACA GCACAATAAG AAGTGGATGA TTGCATCGTG 2100
CTCTCGTTTG TAGGTCTCTT TTCCTAATCA ACACTATGAT TTTGAAGTAC 2150
GCGTACACGA AGCAAACGGG AAGAGATAAG GAATTAGCAT TGTGAACCTG 2200
ACTGTAATCC TCTCTTCCGG AAAGAGATGA GATGCTATTG CGATGAGAAT 2250
GTACAACTTG CACCTTGAAA TCTTTTTTGA TAATTAGTGC TCAGGGGAGG 2300
GGGGGGGAAG TAGAGAAAGC AAA 2323

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Ala Ala Thr Ala Ala Ala
5

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ala Ala Thr Ala Ala Ala
5

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

His Arg Asp Leu Ala Ala
5

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 2 is valine
or methionine; Xaa in
position 5 is phenylalanine
or tyrosine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Asp Xaa Trp Ser Xaa Gly
5

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 993 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile
1 5 10 15
Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu
20 25 30
Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile
35 40 45
Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn
50 55 60
Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn
65 70 75 80
Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln
85 90 95
Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu
100 105 110
Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
115 120 125
Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
130 135 140

Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
 145 150 155 160
 Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
 165 170 175
 Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
 180 185 190
 Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile
 195 200 205
 Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
 210 215 220
 Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
 225 230 235 240
 Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
 245 250 255
 Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
 260 265 270
 Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser
 275 280 285
 Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg
 290 295 300
 Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
 305 310 315 320
 Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
 325 330 335
 Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
 340 345 350
 Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
 355 360 365
 Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
 370 375 380
 Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
 385 390 395 400
 Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
 405 410 415
 Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
 420 425 430

Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
 435 440 445
 Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln
 450 455 460
 Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
 465 470 475 480
 Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys
 485 490 495
 Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
 500 505 510
 Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro
 515 520 525
 Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Ala Thr Ala Val Ser
 530 535 540
 Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val Val Ala Val Ala Gly
 545 550 555 560
 Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe Ile Ile Gly Arg Arg
 565 570 575
 His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly Asp Glu Glu Leu Tyr
 580 585 590
 Phe His Phe Lys Phe Pro Gly Thr Lys Thr Tyr Ile Asp Pro Glu Thr
 595 600 605
 Tyr Glu Asp Pro Asn Arg Ala Val His Gln Phe Ala Lys Glu Leu Asp
 610 615 620
 Ala Ser Cys Ile Lys Ile Glu Arg Val Ile Gly Ala Gly Glu Phe Gly
 625 630 635 640
 Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Gly Gln Arg Asp Val Ala
 645 650 655
 Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr Glu Lys Gln Arg Arg
 660 665 670
 Asp Phe Leu Cys Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro Asn
 675 680 685
 Val Val His Leu Glu Gly Val Val Thr Arg Gly Lys Pro Val Met Ile
 690 695 700
 Val Ile Glu Phe Met Glu Asn Gly Ala Leu Asp Ala Phe Leu Arg Lys
 705 710 715 720

His Asp Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly
 725 730 735
 Ile Ala Ala Gly Met Arg Tyr Leu Ala Asp Met Gly Tyr Val His Arg
 740 745 750
 Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys
 755 760 765
 Val Ser Asp Phe Gly Leu Ser Arg Val Ile Glu Asp Asp Pro Glu Ala
 770 775 780
 Val Tyr Thr Thr Thr Gly Gly Lys Ile Pro Val Arg Trp Thr Ala Pro
 785 790 795 800
 Glu Ala Ile Gln Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser
 805 810 815
 Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr
 820 825 830
 Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala Ile Glu Glu Gly Tyr
 835 840 845
 Arg Leu Pro Ala Pro Met Asp Cys Pro Ala Gly Leu His Gln Leu Met
 850 855 860
 Leu Asp Cys Trp Gln Lys Asp Arg Ala Glu Arg Pro Lys Phe Glu Gln
 865 870 875 880
 Ile Val Gly Ile Leu Asp Lys Met Ile Arg Asn Pro Ser Ser Leu Lys
 885 890 895
 Thr Pro Leu Gly Thr Cys Ser Arg Pro Leu Ser Pro Leu Leu Asp Gln
 900 905 910
 Ser Thr Pro Asp Phe Thr Ala Phe Cys Ser Val Gly Glu Trp Leu Gln
 915 920 925
 Ala Ile Lys Met Glu Arg Tyr Lys Asp Asn Phe Thr Ala Ala Gly Tyr
 930 935 940
 Asn Ser Leu Glu Ser Val Ala Arg Met Thr Ile Asp Asp Val Met Ser
 945 950 955 960
 Leu Gly Ile Thr Leu Val Gly His Gln Lys Lys Ile Met Ser Ser Ile
 965 970 975
 Gln Thr Met Arg Ala Gln Met Leu His Leu His Gly Thr Gly Ile Gln
 980 985 990
 Val

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 994 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile
 1 5 10 15
 Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu
 20 25 30
 Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile
 35 40 45
 Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn
 50 55 60
 Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn
 65 70 75 80
 Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln
 85 90 95
 Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu
 100 105 110
 Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
 115 120 125
 Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
 130 135 140
 Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
 145 150 155 160
 Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
 165 170 175
 Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
 180 185 190
 Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile
 195 200 205

Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
 210 215 220
 Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
 225 230 235 240
 Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
 245 250 255
 Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
 260 265 270
 Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser
 275 280 285
 Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg
 290 295 300
 Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
 305 310 315 320
 Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
 325 330 335
 Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
 340 345 350
 Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
 355 360 365
 Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
 370 375 380
 Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
 385 390 395 400
 Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
 405 410 415
 Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
 420 425 430
 Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
 435 440 445
 Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln
 450 455 460
 Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
 465 470 475 480
 Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys
 485 490 495

Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
 500 505 510
 Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro
 515 520 525
 Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Gly Lys Met Phe Glu
 530 535 540
 Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val
 545 550 555 560
 Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe
 565 570 575
 Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly
 580 585 590
 Asp Glu Glu Leu Tyr Phe His Cys Thr Lys Thr Tyr Ile Asp Pro Glu
 595 600 605
 Thr Tyr Glu Asp Pro Asn Arg Ala Val His Gln Phe Ala Lys Glu Leu
 610 615 620
 Asp Ala Ser Cys Ile Lys Ile Glu Arg Val Ile Gly Ala Gly Glu Phe
 625 630 635 640
 Gly Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Gly Gln Arg Asp Val
 645 650 655
 Ala Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr Glu Lys Gln Arg
 660 665 670
 Arg Asp Phe Leu Cys Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro
 675 680 685
 Asn Val Val His Leu Glu Gly Val Val Thr Arg Gly Lys Pro Val Met
 690 695 700
 Ile Val Ile Glu Phe Met Glu Asn Gly Ala Leu Asp Ala Phe Leu Arg
 705 710 715 720
 Lys His Asp Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg
 725 730 735
 Gly Ile Ala Ala Gly Met Arg Tyr Leu Ala Asp Met Gly Tyr Val His
 740 745 750
 Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys
 755 760 765
 Lys Val Ser Asp Phe Gly Leu Ser Arg Val Ile Glu Asp Asp Pro Glu
 770 775 780

Ala Val Tyr Thr Thr Thr Gly Gly Lys Ile Pro Val Arg Trp Thr Ala
 785 790 795 800
 Pro Glu Ala Ile Gln Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp
 805 810 815
 Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr Gly Glu Arg Pro
 820 825 830
 Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala Ile Glu Glu Gly
 835 840 845
 Tyr Arg Leu Pro Ala Pro Met Asp Cys Pro Ala Gly Leu His Gln Leu
 850 855 860
 Met Leu Asp Cys Trp Gln Lys Asp Arg Ala Glu Arg Pro Lys Phe Glu
 865 870 875 880
 Gln Ile Val Gly Ile Leu Asp Lys Met Ile Arg Asn Pro Ser Ser Leu
 885 890 895
 Lys Thr Pro Leu Gly Thr Cys Ser Arg Pro Leu Ser Pro Leu Leu Asp
 900 905 910
 Gln Ser Thr Pro Asp Phe Thr Ala Phe Cys Ser Val Gly Glu Trp Leu
 915 920 925
 Gln Ala Ile Lys Met Glu Arg Tyr Lys Asp Asn Phe Thr Ala Ala Gly
 930 935 940
 Tyr Asn Ser Leu Glu Ser Val Ala Arg Met Thr Ile Asp Asp Val Met
 945 950 955 960
 Ser Leu Gly Ile Thr Leu Val Gly His Gln Lys Lys Ile Met Ser Ser
 965 970 975
 Ile Gln Thr Met Arg Ala Gln Met Leu His Leu His Gly Thr Gly Ile
 980 985 990
 Gln Val